

IN THE SPECIFICATION;

Please amend the paragraph beginning on page 17, line 5, as follows:

--Finally, ellipsoidal moment profiling has been performed on a simple decoy set. Fourteen decoys and native structures of this set, with a number of residues greater than one hundred, were obtained from Stanford University ~~downloaded from the Internet at location~~ ~~http://dd.stanford.edu/download.shtml~~. Twenty-eight moment calculations were, therefore, performed. A typical result is shown in FIG. 13. Visual inspection of the figure clearly delineates the difference between the correct or native structure and the decoy structure. Figures for all of the fourteen structures look essentially the same. All native structures exhibit a second-order moment profile similar to what had been obtained for the thirty PDB structures. Consequently, hydrophobic ratios can be calculated and they span the range of values previously found for the thirty. The spatial transition to the hydrophilic exterior of the native structures is significantly amplified by the second-order moment. The decoys do not exhibit this plunge to negative values of the second-order moment, nor is the relatively regular behavior in the protein interior reproduced. Hydrophobic ratios cannot, therefore, be assigned to any of the decoy structures.--